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SEQUENCE LISTING

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<120> NOVEL SERINE PROTEASE

<130> Q85990

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<150> JP2002-223878
<151> 2002-07-31

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<170> PatentIn version 3.1

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<212> DNA
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gaa gtc ccc gct ctg gat gcc gcg tgc tgt cga gcg gcc agc att ggc	96
Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Ser Ile Gly	
20 25 30	
gtg gtg gcc acc agc ctt gtc gtc acc ctg gga gtc ctt ttg gcc	144
Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Ala	
35 40 45	
ttc ctc tct aca cag ggc ttc cac gtg gac cac acg gcc gag ctg cgg	192
Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg	
50 55 60	
gga atc cgg tgg acc agc agt ttg cgg cgg gag acc tcg gac tat cac	240
Gly Ile Arg Trp Thr Ser Ser Leu Arg Arg Glu Thr Ser Asp Tyr His	
65 70 75 80	
cgc acg ctg acg ccc acc ctg gag gca ctg ttt gta agt agt ttt cag	288
Arg Thr Leu Thr Pro Thr Leu Glu Ala Leu Phe Val Ser Ser Phe Gln	
85 90 95	
aag aca gag tta gag gca agc tgc ggt tgc tcg gta ctg aat tat	336
Lys Thr Glu Leu Glu Ala Ser Cys Val Gly Cys Ser Val Leu Asn Tyr	
100 105 110	
agg gat ggg aac tcc agt gtc ctc gta cat ttc cag ctg cac ttt ctg	384

Arg Asp Gly Asn Ser Ser Val Leu Val His Phe Gln Leu His Phe Leu			
115	120	125	
ctg cga ccc ctc cag acg ctg agc ctg ggc ctg gag gag gag cta ttg			432
Leu Arg Pro Leu Gln Thr Leu Ser Leu Gly Leu Glu Glu Glu Leu Leu			
130	135	140	
cag cga ggg atc cg ^g gca agg ctg cg ^g gag cac gg ^c atc tcc ctg gct			480
Gln Arg Gly Ile Arg Ala Arg Leu Arg Glu His Gly Ile Ser Leu Ala			
145	150	155	160
gcc tat ggc aca att gtg tcg gct gag ctc aca ggg aga cat aag gga			528
Ala Tyr Gly Thr Ile Val Ser Ala Glu Leu Thr Gly Arg His Lys Gly			
165	170	175	
ccc ttg gca gaa aga gac ttc aaa tca ggc cgc tgt cca ggg aac tcc			576
Pro Leu Ala Glu Arg Asp Phe Lys Ser Gly Arg Cys Pro Gly Asn Ser			
180	185	190	
ttt tcc tgc ggg aac agc cag tgt gtg acc aag gtg aac ccg gag tgt			624
Phe Ser Cys Gly Asn Ser Gln Cys Val Thr Lys Val Asn Pro Glu Cys			
195	200	205	
gac gac cag gag gac tgc tcc gat ggg tcc gac gag gc ^g cac tgc gag			672
Asp Asp Gln Glu Asp Cys Ser Asp Gly Ser Asp Glu Ala His Cys Glu			
210	215	220	
tgt ggc ttg cag cct gcc tgg agg atg gcc ggc agg atc gtg ggc ggc			720
Cys Gly Leu Gln Pro Ala Trp Arg Met Ala Gly Arg Ile Val Gly Gly			
225	230	235	240
atg gaa gca tcc ccg ggg gag ttt ccg tgg caa gcc agc ctt cga gag			768
Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala Ser Leu Arg Glu			
245	250	255	
aac aag gag cac ttc tgt ggg gcc gcc atc atc aac gcc agg tgg ctg			816
Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn Ala Arg Trp Leu			
260	265	270	
gtg tct gct cac tgc ttc aat gag ttc caa gac ccg acg aag tgg			864
Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp Pro Thr Lys Trp			
275	280	285	
gtg gcc tac gtg ggt gc ^g acc tac ctc agc ggc tcg gag gcc agc acc			912
Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser Glu Ala Ser Thr			
290	295	300	
gtg cgg gcc cag gtg gtc cag atc gtc aag cac ccc ctg tac aac gc ^g			960
Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro Leu Tyr Asn Ala			
305	310	315	320
gac acg gcc gac ttt gac gtg gct gtg ctg gag ctg acc agc cct ctg			1008
Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu Thr Ser Pro Leu			
325	330	335	
cct ttc ggc cgg cac atc cag ccc gtg tgc ctc ccg gct gcc aca cac			1056
Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro Ala Ala Thr His			
340	345	350	
atc ttc cca ccc agc aag aag tgc ctg atc tca ggc tgg ggc tac ctc			1104

Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly Trp Gly Tyr Leu			
355	360	365	
aag gag gac ttc ctg gtc aag cca gag gtg ctg cag aaa gcc act gtg			1152
Lys Glu Asp Phe Leu Val Lys Pro Glu Val Leu Gln Lys Ala Thr Val			
370	375	380	
gag ctg ctg gac cag gca ctg tgt gcc agc ttg tac ggc cat tca ctc			1200
Glu Leu Leu Asp Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu			
385	390	395	400
act gac agg atg gtg tgc gct ggc tac ctg gac ggg aag gtg gac tcc			1248
Thr Asp Arg Met Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser			
405	410	415	
tgc cag ggt gac tca gga gga ccc ctg gtc tgc gag gag ccc tct ggc			1296
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly			
420	425	430	
cgg ttc ttt ctg gct ggc atc gtg agc tgg gga atc ggg tgt gcg gaa			1344
Arg Phe Phe Leu Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Glu			
435	440	445	
gcc cgg cgt cca ggg gtc tat gcc cga gtc acc agg cta cgt gac tgg			1392
Ala Arg Arg Pro Gly Val Tyr Ala Arg Val Thr Arg Leu Arg Asp Trp			
450	455	460	
atc ctg gag gcc acc acc aaa gcc agc atg cct ctg gcc ccc acc atg			1440
Ile Leu Glu Ala Thr Thr Lys Ala Ser Met Pro Leu Ala Pro Thr Met			
465	470	475	480
gct cct gcc cct gcc gcc ccc agc aca gcc tgg ccc acc agt cct gag			1488
Ala Pro Ala Pro Ala Ala Pro Ser Thr Ala Trp Pro Thr Ser Pro Glu			
485	490	495	
agc cct gtg gtc agc acc ccc acc aaa tcg atg cag gcc ctc agt acc			1536
Ser Pro Val Val Ser Thr Pro Thr Lys Ser Met Gln Ala Leu Ser Thr			
500	505	510	
gtg cct ctt gac tgg gtc acc gtt cct aag cta caa ggt att ttc ggg			1584
Val Pro Leu Asp Trp Val Thr Val Pro Lys Leu Gln Gly Ile Phe Gly			
515	520	525	
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Ala Glu Arg			
530			

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Met Glu Pro Thr Val Ala Asp Val His Leu Val Pro Arg Thr Thr Lys
1 5 10 15

Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Ser Ile Gly

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25

30

Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Leu Ala
35 40 45

Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg
50 55 60

Gly Ile Arg Trp Thr Ser Ser Leu Arg Arg Glu Thr Ser Asp Tyr His
65 70 75 80

Arg Thr Leu Thr Pro Thr Leu Glu Ala Leu Phe Val Ser Ser Phe Gln
85 90 95

Lys Thr Glu Leu Glu Ala Ser Cys Val Gly Cys Ser Val Leu Asn Tyr
100 105 110

Arg Asp Gly Asn Ser Ser Val Leu Val His Phe Gln Leu His Phe Leu
115 120 125

Leu Arg Pro Leu Gln Thr Leu Ser Leu Gly Leu Glu Glu Leu Leu
130 135 140

Gln Arg Gly Ile Arg Ala Arg Leu Arg Glu His Gly Ile Ser Leu Ala
145 150 155 160

Ala Tyr Gly Thr Ile Val Ser Ala Glu Leu Thr Gly Arg His Lys Gly
165 170 175

Pro Leu Ala Glu Arg Asp Phe Lys Ser Gly Arg Cys Pro Gly Asn Ser
180 185 190

Phe Ser Cys Gly Asn Ser Gln Cys Val Thr Lys Val Asn Pro Glu Cys
195 200 205

Asp Asp Gln Glu Asp Cys Ser Asp Gly Ser Asp Glu Ala His Cys Glu
210 215 220

Cys Gly Leu Gln Pro Ala Trp Arg Met Ala Gly Arg Ile Val Gly Gly
225 230 235 240

Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala Ser Leu Arg Glu
245 250 255

Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn Ala Arg Trp Leu

260

265

270

Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp Pro Thr Lys Trp
275 280 285

Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser Glu Ala Ser Thr
290 295 300

Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro Leu Tyr Asn Ala
305 310 315 320

Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu Thr Ser Pro Leu
325 330 335

Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro Ala Ala Thr His
340 345 350

Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly Trp Gly Tyr Leu
355 360 365

Lys Glu Asp Phe Leu Val Lys Pro Glu Val Leu Gln Lys Ala Thr Val
370 375 380

Glu Leu Leu Asp Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu
385 390 395 400

Thr Asp Arg Met Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser
405 410 415

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly
420 425 430

Arg Phe Phe Leu Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Glu
435 440 445

Ala Arg Arg Pro Gly Val Tyr Ala Arg Val Thr Arg Leu Arg Asp Trp
450 455 460

Ile Leu Glu Ala Thr Thr Lys Ala Ser Met Pro Leu Ala Pro Thr Met
465 470 475 480

Ala Pro Ala Pro Ala Ala Pro Ser Thr Ala Trp Pro Thr Ser Pro Glu
485 490 495

Ser Pro Val Val Ser Thr Pro Thr Lys Ser Met Gln Ala Leu Ser Thr

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cgcgcgaaac tgctggtcca ccggattcc		29
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cttgcggcga tccctcgctg caatagctcc		30
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